RAW SEQUENCE LISTING ERROR REPORT
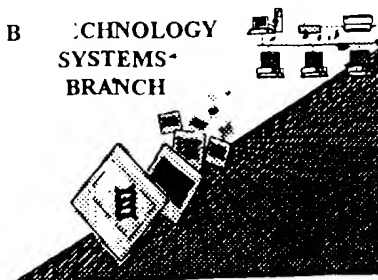
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: __09/806 703__

Source: __PCT__

Date Processed by STIC: __08/30/2001__

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/806703

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

The type of errors shown may exist throughout the Sequence Listing. Please check subsequent sequences for similar errors

PCT09

RAW SEQUENCE LISTING DATE: 08/30/2001
PATENT APPLICATION: US/09/806,703 TIME: 09:49:05

Input Set : A:\3631-109P.ST25.txt
Output Set: N:\CRF3\08302001\I806703.raw

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 3 <110> APPLICANT: Steinaa, Lucilla
 4         Mouritsen, Soren
 5         Gautam, Anand
 6         Dalum, Iben
 7         Haaning, Jesper
 8         Leach, Dana
 9         Nielsen, Klaus
10         Karlsson, Gunilla
11         Rasmussen, Peter
13 <120> TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
15 <130> FILE REFERENCE: 3631-109P
17 <140> CURRENT APPLICATION NUMBER: US 09/806,703
18 <141> CURRENT FILING DATE: 2001-04-04
20 <150> PRIOR APPLICATION NUMBER: PCT/DK99/00525
21 <151> PRIOR FILING DATE: 1999-10-05
23 <150> PRIOR APPLICATION NUMBER: DK 1998 01261
24 <151> PRIOR FILING DATE: 1998-10-05
26 <150> PRIOR APPLICATION NUMBER: DK 60/105,011
27 <151> PRIOR FILING DATE: 1998-10-20
29 <160> NUMBER OF SEQ ID NOS: 33
31 <170> SOFTWARE: PatentIn version 3.0
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 2253
35 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (1)..(2253)
42 <220> FEATURE:
43 <221> NAME/KEY: misc_feature
44 <222> LOCATION: (58)..(2253)
45 <223> OTHER INFORMATION: Human PSM'
48 <400> SEQUENCE: 1
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50 Met Xaa Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
51 1               5                   10                  15
53 cgc ccg cgc tgg ctg tgc gct ggg gcg ctg gtg ctg gcg ggt ggc ttc    96
54 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
55              20                  25                  30
57 ttt ctc ctc ggc ttc ctc ttc ggg tgg ttt ata aaa tcc tcc aat gaa   144
58 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
59          35                  40                  45
61 gct act aac att act cca aag cat aat atg aaa gca ttt ttg gat gaa   192
62 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
63      50                  55                  60
65 ttg aaa gct gag aac atc aag aag ttc tta tat aat ttt aca cag ata   240
66 Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
```

```
67 65                   70                  75                 80
69 cca cat tta gca gga aca gaa caa aac ttt cag ctt gca aag caa att    288
70 Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
71               85                  90                  95
73 caa tcc cag tgg aaa gaa ttt ggc ctg gat tct gtt gag cta gca cat    336
74 Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
75               100                 105                 110
77 tat gat gtc ctg ttg tcc tac cca aat aag act cat ccc aac tac atc    384
78 Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
79           115                 120                 125
81 tca ata att aat gaa gat gga aat gag att ttc aac aca tca tta ttt    432
82 Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
83       130                 135                 140
85 gaa cca cct cct cca gga tat gaa aat gtt tcg gat att gta cca cct    480
86 Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
87 145                 150                 155                 160
89 ttc agt gct ttc tct cct caa gga atg cca gag ggc gat cta gtg tat    528
90 Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
91               165                 170                 175
93 gtt aac tat gca cga act gaa gac ttc ttt aaa ttg gaa cgg gac atg    576
94 Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
95           180                 185                 190
97 aaa atc aat tgc tct ggg aaa att gta att gcc aga tat ggg aaa gtt    624
98 Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
99         195                 200                 205
101 ttc aga gga aat aag gtt aaa aat gcc cag ctg gca ggg gcc aaa gga    672
102 Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
103     210                 215                 220
105 gtc att ctc tac tcc gac cct gct gac tac ttt gct cct ggg gtg aag    720
106 Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
107 225                 230                 235                 240
109 tcc tat cca gat ggt tgg aat ctt cct gga ggt ggt gtc cag cgt gga    768
110 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
111               245                 250                 255
113 aat atc cta aat ctg aat ggt gca gga gac cct ctc aca cca ggt tac    816
114 Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
115           260                 265                 270
117 cca gca aat gaa tat gct tat agg cgt gga att gca gag gct gtt ggt    864
118 Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
119           275                 280                 285
121 ctt cca agt att cct gtt cat cca att gga tac tat gat gca cag aag    912
122 Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
123     290                 295                 300
125 ctc cta gaa aaa atg ggt ggc tca gca cca cca gat agc agc tgg aga    960
126 Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
127 305                 310                 315                 320
129 gga agt ctc aaa gtg ccc tac aat gtt gga cct ggc ttt act gga aac    1008
130 Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
131               325                 330                 335
```

RAW SEQUENCE LISTING   DATE: 08/30/2001
PATENT APPLICATION: US/09/806,703   TIME: 09:49:05

Input Set : A:\3631-109P.ST25.txt
Output Set: N:\CRF3\08302001\I806703.raw

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133 ttt tct aca caa aaa gtc aag atg cac atc cac tct acc aat gaa gtg   1056
134 Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
135         340             345             350
137 aca aga att tac aat gtg ata ggt act ctc aga gga gca gtg gaa cca   1104
138 Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
139         355             360             365
141 gac aga tat gtc att ctg gga ggt cac cgg gac tca tgg gtg ttt ggt   1152
142 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
143         370             375             380
145 ggt att gac cct cag agt gga gca gct gtt gtt cat gaa att gtg agg   1200
146 Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
147 385             390             395             400
149 agc ttt gga aca ctg aaa aag gaa ggg tgg aga cct aga aga aca att   1248
150 Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
151             405             410             415
153 ttg ttt gca agc tgg gat gca gaa gaa ttt ggt ctt ctt ggt tct act   1296
154 Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
155             420             425             430
157 gag tgg gca gag gag aat tca aga ctc ctt caa gag cgt ggc gtg gct   1344
158 Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
159         435             440             445
161 tat att aat gct gac tca tct ata gaa gga aac tac act ctg aga gtt   1392
162 Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
163         450             455             460
165 gat tgt aca ccg ctg atg tac agc ttg gta cac aac cta aca aaa gag   1440
166 Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
167 465             470             475             480
169 ctg aaa agc cct gat gaa ggc ttt gaa ggc aaa tct ctt tat gaa agt   1488
170 Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
171             485             490             495
173 tgg act aaa aaa agt cct tcc cca gag ttc agt ggc atg ccc agg ata   1536
174 Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
175             500             505             510
177 agc aaa ttg gga tct gga aat gat ttt gag gtg ttc ttc caa cga ctt   1584
178 Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
179             515             520             525
181 gga att gct tca ggc aga gca cgg tat act aaa aat tgg gaa aca aac   1632
182 Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
183         530             535             540
185 aaa ttc agc ggc tat cca ctg tat cac agt gtc tat gaa aca tat gag   1680
186 Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
187 545             550             555             560
189 ttg gtg gaa aag ttt tat gat cca atg ttt aaa tat cac ctc act gtg   1728
190 Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
191             565             570             575
193 gcc cag gtt cga gga ggg atg gtg ttt gag cta gcc aat tcc ata gtg   1776
194 Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
195         580             585             590
197 ctc cct ttt gat tgt cga gat tat gct gta gtt tta aga aag tat gct   1824
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RAW SEQUENCE LISTING   DATE: 08/30/2001
PATENT APPLICATION: US/09/806,703   TIME: 09:49:05

Input Set : A:\3631-109P.ST25.txt
Output Set: N:\CRF3\08302001\I806703.raw

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198 Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
199         595                 600                 605
201 gac aaa atc tac agt att tct atg aaa cat cca cag gaa atg aag aca    1872
202 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
203         610                 615                 620
205 tac agt gta tca ttt gat tca ctt ttt tct gca gta aag aat ttt aca    1920
206 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
207 625                 630                 635                 640
209 gaa att gct tcc aag ttc agt gag aga ctc cag gac ttt gac aaa agc    1968
210 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
211                 645                 650                 655
213 aac cca ata gta tta aga atg atg aat gat caa ctc atg ttt ctg gaa    2016
214 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
215         660                 665                 670
217 aga gca ttt att gat cca tta ggg tta cca gac agg cct ttt tat agg    2064
218 Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
219         675                 680                 685
221 cat gtc atc tat gct cca agc agc cac aac aag tat gca ggg gag tca    2112
222 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
223         690                 695                 700
225 ttc cca gga att tat gat gct ctg ttt gat att gaa agc aaa gtg gac    2160
226 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
227 705                 710                 715                 720
229 cct tcc aag gcc tgg gga gaa gtg aag aga cag att tat gtt gca gcc    2208
230 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
231                 725                 730                 735
233 ttc aca gtg cag gca gct gca gag act ttg agt gaa gta gcc taa        2253
234 Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
235                 740                 745                 750
238 <210> SEQ ID NO: 2
239 <211> LENGTH: 750
240 <212> TYPE: PRT
241 <213> ORGANISM: Homo sapiens
243 <220> FEATURE:
244 <221> NAME/KEY: misc_feature
245 <222> LOCATION: (58)..(2253)
246 <223> OTHER INFORMATION: Human PSM'
248 <400>  SEQUENCE: 2
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W--> **250 Met Xaa Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg**
```
251 1                   5                   10                  15
254 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
255         20                  25                  30
258 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
259         35                  40                  45
262 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
263         50                  55                  60
266 Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
267 65                  70                  75                  80
270 Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
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— Errored: When unknowns are included in a sequence listing, they must be enumerated in fields 221, 222, 223.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/806,703

DATE: 08/30/2001
TIME: 09:49:05

Input Set : A:\3631-109P.ST25.txt
Output Set: N:\CRF3\08302001\I806703.raw

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271                85                90                95
274 Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
275                100                105               110
278 Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
279            115                120                125
282 Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
283        130                135                140
286 Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
287 145                150                155                160
290 Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
291                165                170                175
294 Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
295                180                185                190
298 Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
299            195                200                205
302 Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
303        210                215                220
306 Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
307 225                230                235                240
310 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
311                245                250                255
314 Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
315                260                265                270
318 Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
319            275                280                285
322 Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
323        290                295                300
326 Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
327 305                310                315                320
330 Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
331                325                330                335
334 Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
335            340                345                350
338 Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
339        355                360                365
342 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
343        370                375                380
346 Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
347 385                390                395                400
350 Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
351            405                410                415
354 Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
355            420                425                430
358 Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
359        435                440                445
362 Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
363        450                455                460
366 Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
367 465                470                475                480
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VERIFICATION SUMMARY

DATE: 08/30/2001

PATENT APPLICATION: US/09/806,703

TIME: 09:49:06

Input Set : **A:\3631-109P.ST25.txt**
Output Set: **N:\CRF3\08302001\I806703.raw**

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L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:2070 M:283 W: Missing Blank Line separator, <220> field identifier
L:2101 M:283 W: Missing Blank Line separator, <220> field identifier
L:2166 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:2166 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2166 M:283 W: Missing Blank Line separator, <400> field identifier
L:2176 M:283 W: Missing Blank Line separator, <220> field identifier
L:2194 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:2194 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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